

SEQUENCE LISTING

<110> Mr. Hitoshi ENDO

<120> ORGANIC ANION TRANSPORTER AND GENE CODING FOR THE SAME

<160> 2

<210> 1

<211> 2294

<212> DNA

<213> Rat

<223> Number of Chain : Doubled-Stranded

Topology : Linear

Kind : cDNA to mRNA

GCTCCAGCAG	ACCCGTGAAAG	CTGAGCTGTC	CAGACCCCCG	AAGTGAAGAA	AAGAGGGCGAG	60									
GGCAAGGGAG	GGCCAGAACCC	GAGGGAGAGA	GAAAGGAGGG	GCAGCCACC	AGCCCGCTGT	120									
CCTGCCACAG	AACCGGCTCA	GCTCCAGCTC	CAGGAGTCAC	TCAGCTGCAG	AGGCAGTGGC	180									
AGCCCCACTC	CTCAGGCAGAA	GGGCAGCAGA	CAGACAGACA	GAGGTCTAG	GACTGGAGGT	240									
CCTCAGTCAT	TGACCACTCA	GCCTGGCCCA	GCCCC			275									
ATG	GCC	TTC	AAT	GAC	CTC	CTG	AAA	CAG	GTG	GGG	GGC	GTC	GGA	CGC	320
Met	Ala	Phe	Asn	Asp	Leu	Leu	Lys	Gln	Val	Gly	Gly	Val	Gly	Arg	
1	5	10	15												
TTC	CAG	TTG	ATC	CAG	GTC	ACC	ATG	GTG	GTT	GCT	CCC	CTA	CTG	CTG	365
Phe	Gln	Leu	Ile	Gln	Val	Thr	Met	Val	Val	Ala	Pro	Leu	Leu	Leu	
20	25	30													
ATG	GCT	TCC	CAC	AAC	ACC	TTG	CAG	AAC	TTC	ACT	GCC	GCT	ATC	CCC	410
Met	Ala	Ser	His	Asn	Thr	Leu	Gln	Asn	Phe	Thr	Ala	Ala	Ile	Pro	
35	40	45													

CCT CAT CAC TGC CGC CCA CCT GCC AAT GCC AAT CTC AGC AAA GAT	455
Pro His His Cys Arg Pro Pro Ala Asn Ala Asn Leu Ser Lys Asp	
50 55 60	
GGA GGT CTG GAG GCC TGG CTG CCC CTG GAC AAG CAA GGA CAA CCC	500
Gly Gly Leu Glu Ala Trp Leu Pro Leu Asp Lys Gln Gly Gln Pro	
65 70 75	
GAA TCG TGC CTC CGC TTT ACT TCC CCC CAG TGG GGA CCA CCC TTT	545
Glu Ser Cys Leu Arg Phe Thr Ser Pro Gln Trp Gly Pro Pro Phe	
80 85 90	
TAC AAT GGC ACA GAA GCC AAT GGC ACC AGA GTC ACA GAG CCC TGC	590
Tyr Asn Gly Thr Glu Ala Asn Gly Thr Arg Val Thr Glu Pro Cys	
95 100 105	
ATT GAT GGC TGG GTC TAT GAC AAC AGC ACC TTC CCT TCA ACC ATC	635
Ile Asp Gly Trp Val Tyr Asp Asn Ser Thr Phe Pro Ser Thr Ile	
110 115 120	
GTG ACT GAG TGG AAC CTT GTG TGC TCT CAT CGG GCT TTC CGC CAG	680
Val Thr Glu Trp Asn Leu Val Cys Ser His Arg Ala Phe Arg Gln	
125 130 135	
CTG GCC CAG TCC CTG TAC ATG GTG GGA GTG CTG CTG GGA GCC ATG	725
Leu Ala Gln Ser Leu Tyr Met Val Gly Val Leu Leu Gly Ala Met	
140 145 150	
GTG TTT GGC TAC CTG GCG GAC AGG CTG GGC CGC CGG AAG GTG CTG	770
Val Phe Gly Tyr Leu Ala Asp Arg Leu Gly Arg Arg Lys Val Leu	
155 160 165	
ATC TTG AAC TAC CTG CAG ACA GCT GTG TCG GGA ACC TGT GCA GCC	815
Ile Leu Asn Tyr Leu Gln Thr Ala Val Ser Gly Thr Cys Ala Ala	
170 175 180	
TAT GCA CCC AAC TAT ACT GTC TAC TGC GTT TTC CGG CTC CTC TCG	860

Tyr	Ala	Pro	Asn	Tyr	Thr	Val	Tyr	Cys	Val	Phe	Arg	Leu	Leu	Ser	
															185
															190
															195
GGC	ATG	TCT	TTG	GCT	AGC	ATT	GCA	ATC	AAC	TGC	ATG	ACA	CTA	AAT	905
Gly	Met	Ser	Leu	Ala	Ser	Ile	Ala	Ile	Asn	Cys	Met	Thr	Leu	Asn	
															200
															205
															210
GTG	GAA	TGG	ATG	CCT	ATC	CAC	ACC	CGT	GCC	TAT	GTG	GGC	ACC	TTG	950
Val	Glu	Trp	Met	Pro	Ile	His	Thr	Arg	Ala	Tyr	Val	Gly	Thr	Leu	
															215
															220
															225
ATT	GGC	TAT	GTC	TAC	AGC	CTG	GGC	CAG	TTC	CTC	CTG	GCT	GGC	ATC	995
Ile	Gly	Tyr	Val	Tyr	Ser	Leu	Gly	Gln	Phe	Leu	Leu	Ala	Gly	Ile	
															230
															235
															240
GCC	TAT	GCT	GTG	CCC	CAC	TGG	CGC	CAC	CTG	CAG	CTT	GTG	GTC	TCT	1040
Ala	Tyr	Ala	Val	Pro	His	Trp	Arg	His	Leu	Gln	Leu	Val	Val	Ser	
															245
															250
															255
GTG	CCT	TTT	TTC	ATT	GCC	TTC	ATC	TAC	TCT	TGG	TTC	TTC	ATT	GAG	1085
Val	Pro	Phe	Phe	Ile	Ala	Phe	Ile	Tyr	Ser	Trp	Phe	Phe	Ile	Glu	
															260
															265
															270
TCA	GCC	CGC	TGG	TAC	TCC	TCC	TCA	GGA	AGG	CTG	GAC	CTC	ACC	CTC	1130
Ser	Ala	Arg	Trp	Tyr	Ser	Ser	Ser	Gly	Arg	Leu	Asp	Leu	Thr	Leu	
															275
															280
															285
CGA	GCC	CTG	CAG	AGA	GTG	GCC	CGG	ATC	AAT	GGG	AAA	CAA	GAA	GAA	1175
Arg	Ala	Leu	Gln	Arg	Val	Ala	Arg	Ile	Asn	Gly	Lys	Gln	Glu	Glu	
															290
															295
															300
GGG	GCT	AAG	CTA	AGT	ATA	GAG	GTG	CTC	CGG	ACC	AGC	CTG	CAG	AAG	1220
Gly	Ala	Lys	Leu	Ser	Ile	Glu	Val	Leu	Arg	Thr	Ser	Leu	Gln	Lys	
															305
															310
															315
GAA	CTG	ACT	CTA	AGC	AAA	GGC	CAA	GCC	TCA	GCC	ATG	GAG	CTG	CTG	1265
Glu	Leu	Thr	Leu	Ser	Lys	Gly	Gln	Ala	Ser	Ala	Met	Glu	Leu	Leu	

320	325	330	
CGC TGC CCC ACC CTT CGA CAC CTC TTC CTC TGT CTC TCC ATG CTG			1310
Arg Cys Pro Thr Leu Arg His Leu Phe Leu Cys Leu Ser Met Leu			
335	340	345	
TGG TTT GCC ACT AGC TTT GCC TAC TAC GGG CTG GTC ATG GAC CTG			1355
Trp Phe Ala Thr Ser Phe Ala Tyr Tyr Gly Leu Val Met Asp Leu			
350	355	360	
CAG GGC TTT GGG GTC AGC ATG TAC CTT ATC CAG GTG ATT TTC GGT			1400
Gln Gly Phe Gly Val Ser Met Tyr Leu Ile Gln Val Ile Phe Gly			
365	370	375	
GCC GTG GAC CTG CCT GCC AAG TTT GTA TGC TTC CTA GTC ATC AAC			1445
Ala Val Asp Leu Pro Ala Lys Phe Val Cys Phe Leu Val Ile Asn			
380	385	390	
TCC ATG GGG CGC CGG CCT GCA CAG ATG GCC TCC CTG CTG CTG GCA			1490
Ser Met Gly Arg Arg Pro Ala Gln Met Ala Ser Leu Leu Ala			
395	400	405	
GGC ATC TGC ATC CTG GTG AAT GGC ATA ATA CCG AAG AGC CAT ACG			1535
Gly Ile Cys Ile Leu Val Asn Gly Ile Ile Pro Lys Ser His Thr			
410	415	420	
ATC ATT CGC ACC TCC CTG GCT GTG CTA GGG AAG GGC TGC CTG GCT			1580
Ile Ile Arg Thr Ser Leu Ala Val Leu Gly Lys Gly Cys Leu Ala			
425	430	435	
TCC TCT TTC AAC TGC ATC TTC CTG TAC ACC GGA GAG CTG TAC CCC			1625
Ser Ser Phe Asn Cys Ile Phe Leu Tyr Thr Gly Glu Leu Tyr Pro			
440	445	450	
ACA GTG ATT CGG CAG ACA GGC CTG GGC ATG GGC AGC ACC ATG GCC			1670
Thr Val Ile Arg Gln Thr Gly Leu Gly Met Gly Ser Thr Met Ala			
455	460	465	

CGG GTG GGC AGC ATT GTG AGC CCG CTG GTG AGC ATG ACT GCA GAG	470	475	480	1715
Arg Val Gly Ser Ile Val Ser Pro Leu Val Ser Met Thr Ala Glu				
TTC TAC CCC TCC ATG CCT CTC TTC ATC TTC GGC GCT GTC CCT GTG	485	490	495	1760
Phe Tyr Pro Ser Met Pro Leu Phe Ile Phe Gly Ala Val Pro Val				
GTC GCC AGT GCT GTC ACT GCC CTG CTG CCA GAG ACC TTG GGC CAG	500	505	510	1805
Val Ala Ser Ala Val Thr Ala Leu Leu Pro Glu Thr Leu Gly Gln				
CCG CTG CCA GAT ACA GTG CAG GAC CTG AAG AGC AGG AGC AGA GGA	515	520	525	1850
Pro Leu Pro Asp Thr Val Gln Asp Leu Lys Ser Arg Ser Arg Gly				
AAG CAG AAT CAA CAG CAG CAG GAA CAG CAG AAG CAG ATG ATG CCG	530	535	540	1895
Lys Gln Asn Gln Gln Gln Gln Glu Gln Gln Lys Gln Met Met Pro				
CTC CAG GCC TCA ACA CAA GAG AAG AAT GGA CTT	545	550	551	1928
Leu Gln Ala Ser Thr Gln Glu Lys Asn Gly Leu				
TGAGAACGGA AGGGCTTCAC ACAGCACTAA AGGGAGTGGG GTTCTACAGG TCCTGCCGTC	1988			
TACATGAGGA GGGGGAGTGA GTAGAGGGAC TGGACCATCC AAATGTGGAG GCTGCCATT	2048			
AGAGAAATCC CTCCCCAAAG GTCATGTCAG TAGACCCACT AGGAACAAAAA GCTCTGACTA	2108			
TGTGCAGCTT CTTAACGCAGA ATGTTCTCGT CACCGGCCAT CTTCCCTGCTC ATGGTCACTC	2168			
CGCCACCTCC AGGACCTTGC AAAGAATCTC AGACAATTAA ATGAATCTCT TCTAAAAAAA	2228			
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	2288			
AAAAAA				2294

<210> 2

<211> 2171

<212> DNA

<213> Human

<223> Number of Chain : Doubled-Stranded

Topology : Linear

Kind : cDNA to mRNA

GAAAGCTGAG	CTGCCCTGAC	CCCCAAAGTG	AGGAGAAGCT	GCAAGGGAAA	AGGGAGGGAC	60									
AGATCAGGGA	GACCGGGGAA	GAAGGAGGAG	CAGCCAAGGA	GGCTGCTGTC	CCCCCACAGA	120									
GCAGCTCGGA	CTCAGCTCCC	GGAGCAACCC	AGCTGCGGAG	GCAACGGCAG	TGCTGCTCCT	180									
CCAGCGAAGG	ACAGCAGGCA	GGCAGACAGA	CAGAGGTCTT	GGGACTGGAA	GGCCTCAGCC	240									
CCCAGCCACT	GGGCTGGGCC	TGGCCCA				267									
ATG	GCC	TTT	AAT	GAC	CTC	CTG	CAG	GTG	GGG	GGT	GTC	GGC	CGC	312	
Met	Ala	Phe	Asn	Asp	Leu	Leu	Gln	Gln	Val	Gly	Gly	Val	Gly	Arg	
1	5				10				15						
TTC	CAG	CAG	ATC	CAG	GTC	ACC	CTG	GTG	GTC	CTC	CCC	CTG	CTC	CTG	357
Phe	Gln	Gln	Ile	Gln	Val	Thr	Leu	Val	Val	Leu	Pro	Leu	Leu		
	20				25				30						
ATG	GCT	TCT	CAC	AAC	ACC	CTG	CAG	AAC	TTC	ACT	GCT	GCC	ATC	CCT	402
Met	Ala	Ser	His	Asn	Thr	Leu	Gln	Asn	Phe	Thr	Ala	Ala	Ile	Pro	
	35				40				45						
ACC	CAC	CAC	TGC	CGC	CCG	CCT	GCC	GAT	GCC	AAC	CTC	AGC	AAG	AAC	447
Thr	His	His	Cys	Gly	Pro	Pro	Ala	Asp	Ala	Asn	Leu	Ser	Lys	Asn	
	50				55				60						
GGG	GGG	CTG	GAG	GTC	TGG	CTG	CCC	CGG	GAC	AGG	CAG	GGG	CAG	CCT	492
Gly	Gly	Leu	Glu	Val	Trp	Leu	Pro	Arg	Asp	Arg	Gln	Gly	Gln	Pro	
	65				70				75						
GAG	TCC	TGC	CTC	CGC	TTC	ACC	TCC	CCG	CAG	TGG	GGA	CTG	CCC	TTT	537
Glu	Ser	Cys	Leu	Arg	Phe	Thr	Ser	Pro	Gln	Trp	Gly	Leu	Pro	Phe	

80	85	90	
CTC AAT GGC ACA GAA GCC AAT GGC ACA GGG GCC ACA GAG CCC TGC			582
Leu Asn Gly Thr Glu Ala Asn Gly Thr Gly Ala Thr Glu Pro Cys			
95	100	105	
ACC GAT GGC TGG ATC TAT GAC AAC AGC ACC TTC CCA TCT ACC ATC			627
Thr Asp Gly Trp Ile Tyr Asp Asn Ser Thr Phe Pro Ser Thr Ile			
110	115	120	
GTG ACT GAG TGG GAC CTT GTG TGC TCT CAC AGG GCC CTA CGC CAG			672
Val Thr Glu Trp Asp Leu Val Cys Ser His Arg Ala Leu Arg Gln			
125	130	135	
CTG GCC CAG TCC TTG TAC ATG GTG GGG GTG CTG CTC GGA GCC ATG			717
Leu Ala Gln Ser Leu Tyr Met Val Gly Val Leu Leu Gly Ala Met			
140	145	150	
GTG TTC GGC TAC CTT GCA GAC AGG CTA GGC CGC CGG AAG GTA CTC			762
Val Phe Gly Tyr Leu Ala Asp Arg Leu Gly Arg Arg Lys Val Leu			
155	160	165	
ATC TTG AAC TAC CTG CAG ACA GCT GTG TCA GGG ACC TGC GCA GCC			807
Ile Leu Asn Tyr Leu Gln Thr Ala Val Ser Gly Thr Cys Ala Arg			
170	175	180	
TTC GCA CCC AAC TTC CCC ATC TAC TGC GCC TTC CGG CTC CTC TCG			852
Phe Ala Pro Asn Phe Pro Ile Tyr Cys Ala Phe Arg Leu Leu Ser			
185	190	195	
GGC ATG GCT CTG GCT GGC ATC TCC CTC AAC TGC ATG ACA CTG AAT			897
Gly Met Ala Leu Ala Gly Ile Ser Leu Asn Cys Met Thr Leu Asn			
200	205	210	
GTG GAG TGG ATG CCC ATT CAC ACA CGG GCC TGC GTG GGC ACC TTG			942
Val Glu Trp Met Pro Ile His Thr Arg Ala Cys Val Gly Thr Leu			
215	220	225	

ATT GGC TAT GTC TAC AGC CTG GGC CAG TTC CTC CTG GCT GGT GTG		987
Ile Gly Tyr Val Tyr Ser Leu Gly Gln Phe Leu Leu Ala Gly Val		
230	235	240
GCC TAC GCT GTG CCC CAC TGG CGC CAC CTG CAG CTA CTG GTC TCT		1032
Ala Tyr Ala Val Pro His Trp Arg His Leu Gln Leu Leu Val Ser		
245	250	255
GCG CCT TTT TTT GCC TTC TTC ATC TAC TCC TGG TTC ATT GAG		1077
Ala Pro Phe Phe Ala Phe Phe Ile Tyr Ser Trp Phe Phe Ile Glu		
260	265	270
TCG GCC CGC TGG CAC TCC TCC TCC GGG AGG CTG GAC CTC ACC CTG		1122
Ser Ala Arg Trp His Ser Ser Ser Gly Arg Leu Asp Leu Thr Leu		
275	280	285
AGG GCC CTG CAG AGA GTC GCC CGG ATC AAT GGG AAG CGG GAA GAA		1167
Arg Ala Leu Gln Arg Val Ala Arg Ile Asn Gly Lys Arg Glu Glu		
290	295	300
GGA GCC AAA TTG AGT ATG GAG GTA CTC CGG GCC AGT CTG CAG AAG		1212
Gly Ala Lys Leu Ser Met Glu Val Leu Arg Ala Ser Leu Gln Lys		
305	310	315
GAG CTG ACC ATG GGC AAA GGC CAG GCA TCG GCC ATG GAG CTG CTG		1257
Glu Leu Thr Met Gly Lys Gly Gln Ala Ser Ala Met Glu Leu Leu		
320	325	330
CGC TGC CCC ACC CTC CGC CAC CTC TTC CTC TGC CTC TCC ATG CTG		1302
Arg Cys Pro Thr Leu Arg His Leu Phe Leu Cys Leu Ser Met Leu		
335	340	345
TGG TTT GCC ACT AGC TTT GCA TAC TAT GGG CTG GTC ATG GAC CTG		1347
Trp Phe Ala Thr Ser Phe Ala Tyr Tyr Gly Leu Val Met Asp Leu		
350	355	360
CAG GGC TTT GGA GTC AGC ATC TAC CTA ATC CAG GTG ATC TTT GGT		1392

Gln	Gly	Phe	Gly	Val	Ser	Ile	Tyr	Leu	Ile	Gln	Val	Ile	Phe	Gly			
															365	370	375
GCT	GTG	GAC	CTG	CCT	GCC	AAG	CTT	GTG	GGC	TTC	CTT	GTC	ATC	AAC			1437
Ala	Val	Asp	Leu	Pro	Ala	Lys	Leu	Val	Gly	Phe	Leu	Val	Ile	Asn			
															380	385	390
TCC	CTG	GGT	CGC	CGG	CCT	GCC	CAG	ATG	GCT	GCA	CTG	CTG	CTG	GCA			1482
Ser	Leu	Gly	Arg	Arg	Pro	Ala	Gln	Met	Ala	Ala	Leu	Leu	Leu	Ala			
															395	400	405
GGC	ATC	TGC	ATC	CTG	CTC	AAT	GGG	GTG	ATA	CCC	CAG	GAC	CAG	TCC			1527
Gly	Ile	Cys	Ile	Leu	Leu	Asn	Gly	Val	Ile	Pro	Gln	Asp	Gln	Ser			
															410	415	420
ATT	GTC	CGA	ACC	TCT	CTT	GCT	GTG	CTG	GGG	AAG	GGT	TGT	CTG	GCT			1572
Ile	Val	Arg	Thr	Ser	Leu	Ala	Val	Leu	Gly	Lys	Gly	Cys	Leu	Ala			
															425	430	435
GCC	TCC	TTC	AAC	TGC	ATC	TTC	CTG	TAT	ACT	GGG	GAA	CTG	TAT	CCC			1617
Ala	Ser	Phe	Asn	Cys	Ile	Phe	Leu	Tyr	Thr	Gly	Glu	Leu	Tyr	Pro			
															440	445	450
ACA	ATG	ATC	CGG	CAG	ACA	GGC	ATG	GGA	ATG	GGC	AGC	ACC	ATG	GCC			1662
Thr	Met	Ile	Arg	Gln	Thr	Gly	Met	Gly	Met	Gly	Ser	Thr	Met	Ala			
															455	460	465
CGA	GTG	GGC	AGC	ATC	GTG	AGC	CCA	CTG	GTG	AGC	ATG	ACT	GCC	GAG			1707
Arg	Val	Gly	Ser	Ile	Val	Ser	Pro	Leu	Val	Ser	Met	Thr	Ala	Glu			
															470	475	480
CTC	TAC	CCC	TCC	ATG	CCT	CTC	TTC	ATC	TAC	GGT	GCT	GTT	CCT	GTG			1752
Leu	Tyr	Pro	Ser	Met	Pro	Leu	Phe	Ile	Tyr	Gly	Ala	Val	Pro	Val			
															485	490	495
GCC	GCC	AGC	GCT	GTC	ACT	GTC	CTC	CTG	CCA	GAG	ACC	CTG	GGC	CAG			1797
Ala	Ala	Ser	Ala	Val	Thr	Val	Leu	Leu	Pro	Glu	Thr	Leu	Gly	Gln			

500 505 510  
CCA CTG CCA GAC ACG GTG CAG GAC CTG GAG AGC AGG TGG GCC CCC 1842  
Pro Leu Pro Asp Thr Val Gln Asp Leu Glu Ser Arg Trp Ala Pro  
515 520 525  
ACT CAG AAA GAA GCA GGG ATA TAT CCC AGG AAA GGG AAA CAG ACG 1887  
Thr Gln Lys Glu Ala Gly Ile Tyr Pro Arg Lys Gly Lys Gln Thr  
530 535 540  
CGA CAG CAA CAA GAG CAC CAG AAG TAT ATG GTC CCA CTG CAG GCC 1932  
Arg Gln Gln Gln Glu His Gln Lys Tyr Met Val Pro Leu Gln Ala  
545 550 555  
TCA GCA CAA GAG AAG AAT GGA CTC 1956  
Ser Ala Gln Glu Lys Asn Gly Leu  
560 563  
TGAGGACTGA GAAGGGGCCT TACAGAACCC TAAAGGGAGG GAAGGTCCCTA CAGGTCTCCG 2016  
GCCACCCACA CAAGGAGGAG GAAGAGGAAA TGGTGACCCA AGTGTGGGGG TTGTGGTTCA 2076  
GGAAAGCATC TTCCCAGGGG TCCACCTCCC TTTATAAACCC CCACCAGAAC CACATCATTA 2136  
AAAGGTTTGA CTGCGAAAAA AAAAAAAA AAAAA 2171